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; SEQUENCE DESCRIPTION: SEQ ID NO: 6348:
US-09-107-532A-6348
                                                                                               January 30, 2004, 15:23:07; Search time 21 Seconds (without alignments) 1124.260 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6348, Ap
Sequence 5060, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Appli
Sequence 5311, Ap
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                                                                                                                                                              US-10-037-311B-1
3004
1 MDQNSYRRRSSPIRTITGGS......GTLVPHVRHCEDISWGLKLV 558
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Sequence 3
Sequence 6
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Sequence 2
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Sequence 6
Sequence 1
Sequence 2
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-134-001C-5060
US-09-252-91A-31996
US-08-836-687B-30
US-09-186-276B-58
US-08-842-445-58
US-09-186-276B-58
US-09-186-188B-58
US-09-489-847-352
US-09-222-617A-12
US-08-222-617A-27
US-08-222-617A-27
US-08-222-617A-27
US-08-222-617A-27
US-08-222-617A-27
US-08-222-617A-27
US-08-226-17A-27
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                                                                                                                                                                                                                                                                                   328717 seqs, 42310858 residues
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Maximum Match 100%
Listing first 45 summaries
                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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Sequence 7, Appli Sequence 7, Appli Sequence 5, Appli Sequence 5, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 33, Appli Sequence 33, Appli Sequence 33, Appli Sequence 32, Appli Sequence 32, Appli Sequence 33, Appli Sequence 32, Appli		and David Bush AND AMINO ACID SEQUENCES RELATING TO FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS CS CORPORATION	
584 1 US-08-179-738-7 584 2 US-08-628-145-7 591 1 US-08-628-145-5 596 1 US-08-179-738-5 596 1 US-08-179-738-5 596 2 US-08-628-145-5 597 2 US-08-179-738-2 777 2 US-08-179-738-3 777 4 US-09-844-678-3 777 4 US-09-348-886-3 777 4 US-09-346-648-3 1298 1 US-08-222-616-3 1298 4 US-08-901-710-2 298 4 US-08-914-648-3 1363 2 US-08-874-678-3 1363 2 US-08-874-678-3	ALIGNMENTS	H	COUNTER: USBACK COUNTER: USBACK TER READABLE FORM: MEDIUM TYPE: CD/ROM ISO9660 COMPUTER: PC OPERATING SYSTEM: <unknown> SOFTWARE: ASCII APPLICATION DATA: APPLICATION NUMBER: US/09/107,532A APPLICATION NUMBER: 06/085,598 FILING DATE: 30-Jun-1998 APPLICATION NUMBER: 60/085,598 FILING DATE: 14 May 1998 APPLICATION NUMBER: 60/08171 INEY/AGBNT INFORMATION: NAME: Ariniello, Pamela Deneke FILING DATE: July 2, 1997 INEY/AGBNT INFORMATION: NAME: Ariniello, Pamela Deneke REGISTRATION NUMBER: 40,489 REFERENCE/DOCKET NUMBER: GTC-012 COMMUNICATION INFORMATION: NEC CHARACTERISTICS: LEBERAX: (781)893-8077 N FOR SEQ ID NO: 6348: NAL SOURCE: ORGANISM: Enterococcus faecium RE: NAME/KEY: misc feature NAME/KEY: misc feature</unknown>
28 85 2.8 85 2.8 31 32 33 33 34 48 85 2.8 55 34 34 42 85 2.8 77 42 85 2.8 128 43 85 2.8 128 44 85 2.8 128 45 85 85 85 85 85 85 85 85 85 85 85 85 85		RESULT 1 US-09-107-532A-6348 Sequence 6349, Application US/09107532A Patent No. 6583275 Patent No. 6583275 TILE OF INVENTION: NUCLEIC ACID ENTEROCOCCUS NUMBER OF SEQUENCES: 7310 CORRESPONDENCE ADDRESS: ADDRESSES: GENOME THERAPEUT STREET: 100 Beaver Street CITY: Waltham STREET: AND ADDRESSES CITY: Waltham STREET: AND SEACHUSETES	COMPUTRY: USA COMPUTRY: USA COMPUTER READABLE FORM: MEDIUM TYPE: CD/ROM ISO9 COMPUTER: PC FILING DATE: 14 May 1998 APPLICATION NUMBER: 60/0 FILING DATE: 14 May 1998 FERFERNCE/DOCKET NUMBER: PROPERTICAL: YES ORIGINAL SOURCE: COMPUTER: MAME/KEY: MISC FEALURE LOCATION: (B) LOCATION 1 SEQUENCE DESCRIPTION: SEO 1D N

us-10-037-311b-1.rai

Db 279 PL-FNLTDLOQEAYRRYKOMGPKETLANTLQHLYERHKLVTYPRTDSNYLTDDM 329 Qy 286 QTFIGKVPWLIVKTDNYFVPSLWLIPGFDDELNKLPPQKATVFHH 330	Qy 504 NRTTPD-PSCGRAMSWEPCFHSPFYDCKAKTGIDTGT 540	FALON FILING DAILE: 1998-07-27	197 LLTDRVLLVDRGKDMDDLFCEPFLGMSWLLPLDFPMTDGFDGL 197 LLTDRV
Query Match 3.7%; Score 111.5; DB 4; Length 804; Best Local Similarity 21.4%; Pred. No. 0.019; Matches 101; Conservative 61; Mismatches 132; Indels 179; Gaps 26; Qy	Db 367 LPDPTVVLRRFFEDERNBDYLP-LIDEAHNLVNRSREMYSAELSYEK 412 Qy 359 EKIGIQVRVFDEDPGPFQHVMDQISSCTQKEKLLPEVDTLVERSRHVNTPKHKAVLVT 416	JUNEARLY INFORMATION: JUNEARLY INFORMATION: TITLE OF INVENTION: BEDDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS TITLE OF INVENTION: BEDDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS TURENT FILE SEPERANCE: GTC-007 CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR PILING DATE: 1997-01-08 PRIOR PILING DATE: 1997-08-14 NUMBER OF SEQ ID NOS: 5674 SEQ ID NO 5060 LENGTH: 723 TYPE: PRT	

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NAME/KEY: VARIANT
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SEQ ID NO 58
LENGTH: 809
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                                                                                                                                                                                                                                                                                                                                                                    224 ISNLQKD-----LLSDFSWNTFLTKVEAIDEDKKYIIPLKKVQKFIQEYSEIE----I 272
                                                                                                                                                                                                                                                                                                                                                                                                                        147 GPGTESYKKALKQLDQ------EHIDGDGECKYVVWISPSGLGNRILSLAS 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                             273 GEĞIEKLKEIYQEMSĞILENDNYIQIDLISDSEİNFDVKOKOQLEHLAEFLĞNTTKSVRR 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192 VFL--YALLTDRVLL---VDRGKDMDDLFCEPFLGMSWLLPLDFPMTDQFDG-----LN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             333 TYLDDY----KDKFIEKYGVDQEVQITELFDSTF--GIGAPYNYNHPRNDFYESEPSTLYYS 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 QESSRCYGYM----VKN-QVIDTEGTLSH---------LYLHLVHDYGDHDKM 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 280 PPCEGDQTFIGKVPWLIVKTDNYFVPSLWLIPGPDDELNKLFPQKATVFHHLGRYLFHPT 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              340 NQVWGLVTRYYEAYLSHADEKIGIQVRVFDEDPGPFQHVMDQISSCTQKEKLLPEVDTLV 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89 VTNINSDKLLGGLLASGFDEDSCLSRYQSVHYRKP--SPYKPSSYLISKLRNYEKLHKRC
                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Benefey, Philip
APPLICANT: Bilaurenzio Laura
APPLICANT: Bilaurenzio Laura
APPLICANT: Wagocka-Diller, Joanna
APPLICANT: Walamy, Jocelyn E.
APPLICANT: Pysh, Leonard
FILE REFERENCE: 5914-075-999
CURRENT PRILING DATE: 1998-1-05
FRIOR APPLICATION NUMBER: 08/642,445
FRIOR APPLICATION NUMBER: 08/638,617
FRIOR APPLICATION NUMBER: 08/638,617
FRIOR APPLICATION NUMBER: 08/638,617
FRIOR PILING DATE: 1996-04-26
NUMBER OF SEQ ID NOS: 79
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 58
LENGTH: 809
                                                                                                                                                                                                                                                                                                    Indels 167;
                                                                                                                                                                                                                                                               DB 4; Length 993
                                                                                                                                                                                                                                                             Query Match
3.1%; Score 92.5; DB 4; I
Best Local Similarity 19.1%; Pred. No. 2.7;
Matches 90; Conservative 63; Mismatches 152;
APPLICANT: Dodd, Helen Mair
TITLE OF INVENTION: PRODUCTION OF VARIANT NISIN
FILE REPERENCE: 2014/70
CURRENT APPLICATION NUMBER: US/08/836,687B
CURRENT PILING DATE: 1995-11-20
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 30
LENGTH: 993
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US-09-186-276B-58
Sequence 58, Application US/09186276B
Patent No. 6388173
GENERAL INFORMATION:

    TYPE: PRT
    ORGANISM: Lactococcus sp.
US-08-836-6878-30

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63 PPSSNQTLGLANGFYLDDLDFSSLDPPEAYPSQNNNNNNINNKAVAGDLLSSSSDDADFS 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                222 WIHTPMPSNF----VPQSTSRSNSVTGGGGGGNSAVYGSGFGDDLVSNMFKD--DELAMQ 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | | | : : | : : : : | | : | | : | 332 YAPPPNRLTGKKSHWRDEDEDFVEERSNKQSAVYVEE-SELSEMFDNMFLCGPGKPVC-- 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSDSNRIMGFAEARVLD-----AGVFP----NVTNINSDKLLGGLLASGFDE---- 108
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                                                                                                                                                                                                                                                                                                                            66 PSDSNRIMGFAEARVLD-----AGVFP----NVTNINSDKLLGGLLASGFDE---- 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 SHSPDGSCS------GGAFSDYAS------TTTTTSSDSHWSVDGLENRP----S 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 281 FCEGDQ---TFIGKVPWLIVKTDNYFVPSLWLIPGFDDELNKLF---PQKATVFHHLGRY 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   335 LFHPTNQVWGLVTRYYEAYLSHADEKIGIQVRVFDEDPGPFQHVMDQISSCTQKEKLLPE 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 DSCLSRYOSVHYRKPSPYKPSSYLIS-KLRNYEK-LHKRCGPGTESYKKALKQLDQEHI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166 -- DGDGECKYVVWISFSGLGNRILSLASVFLYALLTDRVLLVDRGKDMDDLFCEPFLGMS
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                                                                                                                                                                                                                                                                    72;
                                                                                                                                                                                                            DB 4; Length 809;
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                                                                                                                                                                                                      3.1%; Score 92; DB 4; Length 809
21.7%; Pred. No. 2.2;
ive 52; Mismatches 179; Indels
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3.1%; Score 92; DB 4; Length 809
Best Local Similarity 21.7%; Pred. No. 2.2;
Matches 84; Conservative 52; Mismatches 179; Indels
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APPLICANT: Benfey et al.
TITLE OF INVENTION: Scarecrow Gene, Promoter and Uses
TITLE OF INVENTION: Thereofor FILE REFERENCE: 5314-056-999
CURRENT APPLICATION NUMBER: US/08/842,445A
CURRENT FILING DATE: 1997-04-24
EARLIER APPLICATION NUMBER: 08/638,617
BARLIER PILING DATE: 1996-04-26
NUMBER OF SEQ ID NOS: 79
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; OTHER INFORMATION: Xaa = Any Amino Acid
US-08-842-445-58
                           FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(809)
COTHER INFORMATION: Xaa = Any Amino Acid
US-09-186-276B-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-842-445-58
; Sequence 58, Application US/08842445A
; Patent No. 6441270
ORGANISM: Arabidopsis thalians
                                                                                                                                                                                                      Query Match
Best Local Similarity 21.74
Matches 84; Conservative
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COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids LOCATION: (109)

COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-489-847-152
                                                                                                                                                                                           332 YAPPPNRLTGKKSHWRDEDEDFVEERSNKQSÅVYVEE-SELSEMFDNMFLCGPGKPVC-- 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 VEECNGRRAKLLACDGNEIDTMFVDRRGTAEPQGQKLV-----ICCEGNAGFY-EV 290
                                                276 PKKGVEEASKFLPKSSQLFIDVDSY-IP---MNSGSKENGSEVFVKTEKKDETEHHHHHS 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------PCQ 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173 YVVWISFSGLGNRILSLASVFLYALLTDRVLLVDRGKDMDDLFCEPFLGMSWLLPLDFPM 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203 ITSYLVAHTLGRRMLYPGSVYLLQKALMPVLLQGQAR---------- 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233 TDQFDGLNQESSRCYGYMVKNQVIDTEGILSHLYLHLVHDYGDHDKMFFCEGDQTFIGKV 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293 PWLIVKTDNYFVPSLWLIPGFDDELNKLPPQKAT------VFHHLGRYLFHPTNQV- 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              291 GCVSTPLEAGYSVLGWNHPGFAGSTGVPFPQNEANAMDVVVQFAIHRLG---FQPQDIII 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---W-GLVTRYYEAY--LSH 356
281 FCEGDQ----TFIGKVPWLIVKTDNYFVPSLWLIPGFDDELNKLF---PQKATVFHHLGRY 334
                                                                                                                                          335 LFHPTNQVWGLVTRYYEAYLSHADEKIGIQVRVFDEDPGPFQHVMDQISSCTQKEKLLPE 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
3.0%; Score 91; DB 4; Length 554;
Best Local Similarity 19.6%; Pred. No. 1.5;
Matches 86; Conservative 50; Mismatches 152; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Rosen et al
TILLE OF INVENTION: 98 Human Secreted Proteins
FILE SPERENCE: PZ031P1
CURRENT APPLICATION NUMBER: US/09/489,847
CURRENT APPLICATION NUMBER: US/09/489,847
CURRENT FILING DATE: 2000-01-24
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-29
EARLIER FILING DATE: 1998-08-05
EARLIER FILING DATE: 1998-08-05
EARLIER FILING DATE: 1998-08-05
EARLIER FILING DATE: 1998-08-05
EARLIER FILING DATE: 1998-08-06
EARLIER APPLICATION NUMBER: 60/095,455
EARLIER APPLICATION NUMBER: 60/095,455
EARLIER APPLICATION NUMBER: 60/095,455
EARLIER PILING DATE: 1998-08-06
SARIER PILING DATE: 1098-08-06
SARIER PILING DATE: 1098-08-06
SARIER PILING DATE: 1098-08-06
SARIER PILING DATE: 1098-08-06
SARIER PARESE PARENTING DATE: 1098-08-06
SARIER PILING DATE: 1098-08-06
                                                                                                                                                                                                                                                                                                                                          389 -----ILNQNFPTESAKVVTAQSNG 408
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Patent No. 6476195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             343
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                                                                                                                                                                                                                                                                                                                           224 WL---LPLDFPMTDQFDGLNQESSRCYGYMVKNQVIDTEGTLSHLYLHLVHDYGDHDKMF 280
                                                                                                                                                                                                                                                                                                                                                                            222 WLHTPWPSNF----VFQSTSRSNSVTGGGGGGNSAVYGSGFGDDLVSNMFKD--DELAMQ 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 PPSSNQTLGLANGFYLDDLDFSSLDPPEAYPSQNNNNNNNNNNAVAGBLLSSSSDDADFS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSCLSRYQSVHYRKPSPYKPSSYLIS-KLRNYEK-LHKRCGPGTESYKKALKQLDQEHI- 165
                                                                                                         123 DSVLKYISQVLMEEDMEEKPCMFHDALALQAAEKSLYEALGEKDPSSSSASSVDHPERLA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             281 FCEGDQ---TFIGKVPWLIVKTDNYFVPSLWLIPGFDDELNKLF---PQKATVFHHLGRY 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          335 LFHPTNOVWGLVTRYYEAYLSHADEKIGIQVRVFDEDPGPFQHVMDQISSCTQKEKLLPE 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            332 YAPPPNRLTGKKSHWRDEDEDFVEERSNKQSAVYVEE-SELSEMFDNMFLCGPGKPVC-- 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 DSCLSRYQSVHYRKPSPYKPSSYLIS-KLRNYEK-LHKRCGPGTESYKKALKQLDQEHI- 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 -- DGDGECKYVVWISFSGLGNRILSLASVFLYALLTDRVLLVDRGKDMDDLFCEPFLGMS 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WL---LPLDFPMTDQFDGLNQESSRCYGYMVKNQVIDTEGTLSHLYLHLVHDYGDHDKMF 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               166 -- DGDGECKYVVWISFSGLGNRILSLASVFLYALLTDRVLLVDRGKDMDDLFCEPFLGMS
                                                                                                                                                                                                                                                           183 SHSPDGSCS-----GGAFSDYAS-----TTTTTSSDSHWSVDGLENRP----S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 PSDSNRIMGFAEARVLD-----AGVFP----NVTNINSDKLLGGLLASGFDE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHSPDGSCS-----GGAPSDYAS----TTTTTSSDSHWSVDGLENRP---S
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3.1%; Score 92; DB 4; Length 809;
Best Local Similarity 21.7%; Pred. No. 2.2;
Matches 84; Conservative 52; Mismatches 179; Indels
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US-09-186-188B-58

i Sequence 58, Application US/09186188B

patent No. 6455672

GENERAL INFORMATION:
   APPLICANT: Benfey et al.
   TITLE OF INVENTION: Thereof
   TITLE OF INVENTION: Thereof
   TITLE OF INVENTION: Thereof
   PILE REFREENCE: 5914-074-999
   CURRENT FILING DATE: 1998-11-05
   PRIOR PRILING DATE: 1998-11-05
   PRIOR APPLICATION NUMBER: 08/842,445
   PRIOR APPLICATION NUMBER: 08/638,617
   PRIOR FILING DATE: 1996-04-26
   NUMBER OF SEQ ID NOS: 79
   SEQ ID NOS: 79
   SEQ ID NOS: 79
   LENGTH: 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   395 VDTLVERSRHVNTPKHKAVLVTSLNAG 421
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LOCATION: (1)...(809)
CATER INFORMATION: Xaa = Any Amino Acid
US-09-186-188B-58
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ORGANISM: Plant
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71 RIMGFAEARVLDAGVFPNVTNINSDKLLGGLLASGFDEDSCLSRYQSVHYRKPSPYKPS- 129
                                               ----SKWS----VSNPSPLSRST 168
                                                                                         130 --SYLISKLRNYEKLHKRCGPGTESYKKALKQLDQEHIDGDGECKYVVWISFSGLGNRIL 187
                                                                                                                          169 DLAYIIYT------SGTTGRPKG-------VTVEHHGVVNLQV 198
                                                                                                                                                                                188 SLASVFLYALLTDRVLLVDRGKDMD----DLFCEPFLGMSWLLPLDFPMTDQFDGLNQESS 244
                                                                                                                                                                                                                                                                         245 RCYGYMVKNQVIDTEGTLSHLYLHLVHDYGDHDKMFFCEGD------QTFIGKVP 293
                                                                                                                                                                                                                                                                                                        294 WLIVKTDNYFVPSLWLIPGFDDELNKLFPQKATVFHHLGRYLFHPTNQVWGLVTRYYEAY 353
                                                                                                                                                                                                                          199 ŚLSKVFGLRDTDDEVILSFSNYVFDHFVEOMTDAILNGOTLLVLN------DGMRGDKE 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Martin, Juan F.
APPLICANT: Garcia, Bruno D.
APPLICANT: Gutierrez, Santiago
APPLICANT: Gutierrez, Santiago
APPLICANT: Gutierrez, Santiago
APPLICANT: Barredo, Jose L.
APPLICANT: Palissa, Harriet
APPLICANT: Palissa, Harriet
APPLICANT: Montenegro, Harriet
APPLICANT: Montenegro, Eduardo P.
TITLE OF INVENTION: A Method for Influencing Beta-Lactam
TITLE OF INVENTION: Antibiotic Production and for Isolation of Large
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                             311 -------PBRRM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3: McDonnell Boehnen Hulbert & Berghoff
300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FAPILCATION NUMBER: US/08/222,617A
FILING DATE: 04-APR-1994
CLASSIFICATION: 435
                                               132 RİKGMAASGTL---LYPSVLPANPD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Penicillium chrysogenum
                                                                                                                                                                                                                                                                                                                                                                                                                                                          354 LSHADEKIGIQVR-----VFDED 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      336 ----DKSIGQQVHNSTSYVLNED 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-222-617A-12; Sequence 12, Application US/08222617A; Patent No. 5882879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Veenstra, Annemarie E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 9'
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 3666 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRECT: 300
STREET: 300
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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APPLICANT:
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                                                                        460 EEGLRVVRQWLEASSQLEEASIYSRWEVEEDWCLSVLRSYQAEHGPDFPWSVGEDMSADG 519
348 YAWSIGGFTATWAAMSYPDVSAMILDASFDDLVPLALKVMPDSWRGLVTRTVRQHLNLNN 407
                                          357 ADEKIGIQVRVFDEDPGP---FQHVMDQISSCTQKEKLLPR--VDTLVERSRH----VNT 407
                                                                                                                                   -----YPTSTGEIIGVHQ 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Martin, Juan F.
APPLICANT: Garcia, Bruno D.
APPLICANT: Gutlerrez, Santiago
APPLICANT: Gutlerrez, Santiago
APPLICANT: Barredo, Jose L.
APPLICANT: Von Doehren, Hans
APPLICANT: Von Liempt, Henk
APPLICANT: Wan Liempt, Henk
APPLICANT: Montenegro, Eduardo P.
TITLE OF INVENTION: A Method for Influencing Beta-Lactam
TITLE OF INVENTION: Antibiotic Production and for Isolation of Large
TITLE OF INVENTION: Quantities of ACV Synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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/note= "Domain II of ACV Synthetase from
Penicillium chrysogenum; aa 1397-2154"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
3.0%; Score 90; DB 2; Length 758;
Best Local Similarity 20.7%; Pred. No. 3.2;
Matches 67; Conservative 35; Mismatches 99; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: ISP Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,617A
FILING DATE: 04-APR-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McDonnell Boehnen Hulbert & Berghoff
                                                                                                                               408 PKHKAVLVTSLNAGYAENLKSMY--WE----
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REFERENCE/DOCKET NUMBER: 97,157

INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:

LENGTH: 758 amino acids
   TYPE: amino acids
   TYPE: amino acids
   STRANDEDNESS: single
   TOPOLOGY: linear
   MOLECULE TYPE: protein
   FRAGMENT TYPE: internal
   ORIGINAL SOURCE:
   ORGANISM: Penicillium chrysogenum
   FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08222617A
Patent No. 5882879
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Veenstra, Annemarie E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 300 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                       446 PSQEGYQQTEKKMHNGKA 463
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION: 1..758
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US-08-222-617A-6
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McDonnell Boehnen Hulbert & Berghoff
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CURRENT APPLICATION DATA.
APPLICATION NUMBER: US/08/222,617A
FILING DATE: 04-APR-1994
                                                                                                                                                                                Query Match
3.0%; Score 90; DB 2
Best Local Similarity 20.7%; Pred. No. 44;
Matches 67; Conservative 35; Mismatches
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Barredo, Jose L.
Von Doehren, Hans
Palissa, Harriet
Van Liempt, Henk
Montenegro, Eduardo P.
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OPERATING SYSTEM: PC-DOS/MS-DOS
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Martin, Juan F.
Garcia, Bruno D.
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Patent No. 5882879
GENERAL INFORMATION:
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REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 2
LENGTH: 3727 amino acids
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TITLE OF INVENTION: Ant:
TITLE OF INVENTION: Quar
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCDONNEIL I
                                                         TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-222-617A-27
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STREET: 300
CITY: Chicago
                                      amino acid
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CAPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 SLASVFLYALLTDRVLLVDRGKDMD---DLFCEPFLGMSWLLPLDFPWTDQFDGLNQESS 244
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APPLICANT: Montenegro, Eduardo P.
TITLE OF INVENTION: A Method for Influencing Beta-Lactam
TITLE OF INVENTION: Antibiotic Production and for Isolation of Large
TITLE OF INVENTION: Quantities of ACV Synthetase
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                      Gaps
                                                                /label= region
/note= "Region of ACV Synthetase; aa 62-3727"
                                                                                                                                                                                                                                                35; Mismatches 99; Indels 122;
                                                                                                                                                                             Score 90; DB 2; Length 3666; Pred. No. 43;
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APPLICATION NUMBER: US/08/222,617A
FILING DATE: 04-APR-1994
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OPERATING SYSTEM: PC-DOS/MS-DOS
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REFERENCE/DOCKET NUMBER: 97,157
INFORMATION FOR SEQ ID NO: 27:
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Barredo, Jose L.
Von Doehren, Hans
Palissa, Harriet
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Garcia, Bruno D.
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                                                                                                                                                                                Query Match
Best Local Similarity 20.7*
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                COCATION: 1..3666
CTHER INFORMATION:
CTHER INFORMATION:
US-08-222-617A-12
      NAME/KEY: Protein
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STREET: 30
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US-08-222-617A-27
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1648 KLYRYIEKNRVTYLSGTPSVVSMYBFSRFKDHLRRVDCVGEAFSEPVFDKIRETFHGLV- 1706
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                                                                                                                                 71 RIMGFAEARVLDAGVFPNVTNINSDKLLGGLLASGFDEDSCLSRYQSVHYRKPSPYKPS- 129
                                                                                                                                                                                                                                                                          130 --SYLISKLRNYEKLHKRCGPGTESYKKALKQLDQEHIDGDGECKYVVWISFSGLGNRIL 187
                                                                                                                                                                                                                                                                                                                                                                                                         188 SLASVFLYALLTDRVLLVDRGKDMD----DLFCEPFLGMSWLLPLDFPMTDQFDGLNQESS 244
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Antibiotic Production and for Isolation of Large
Quantities of ACV Synthetase
                                                                      Gaps
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DB 2; Length 3727;
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843 DGIINQRAFYNYLSAWATNDVFAYGASQGKL--YPEPRQYFHQPNEYDLKIPKSLPLVYA 900
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791 E-----EYRDGRLTKECWFPNASSDAILAYKLIVQTGHVDNPVDKELVLTNRLVNS 841
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                                                                       421 GYAENLKSMY------WEYPTSTGELIGVHQPSQEGYQQTEKKMHNGKAL----A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   672 PFLMRSWVKFLTVMGFLAALISSLYASTRLQDGLDIIDLVPKDSNEHKFLDAQTRLFGFY
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                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SCOTT, MATHEW P
APPLICANT: GOODRICH, LISA V
APPLICANT: JOHNSON, RONALD L
ATTLE OF INVENTION: Patched Genes and their Use
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
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STREET: Four Embarcadero Center, Suite 3400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/540,406
FILING DATE: 06-OCT-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM PC compatible
YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                   ; Sequence 6, Application US/08540406
; Patent No. 5837538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: at
TELECOMMUNICATION INFORMATION
TELEPHONE: 415-781-1989
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NAME: Rowland, Bertram I
REGISTRATION NUMBER: 200
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Best Local Similarity 20.39
Matches 63, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                            474
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MEDIUM TYPE: Floppy
                                                                                                                                                        466 EM--YLLSLTD
                                                                                                                                                                                    COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: siz
                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                               1528 RİKGMAASGTL---LYPSVLPANPD------SKWS---VSNPSPLSRST 1564
                                                                                                                                                                                                                                                                                                                                1565 DLAYIIYT-----SGTTGRPKG-------VTVEHHGVVNLQV 1594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1595 ŚLSKVFGLRDTDDEVILSFSNYVFDHFVEQMTDAILNGQTLLVLN------DGMRGDKE 1647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3. Application US/09268140
Patent No. 6268176
GENERAL INFORMATION:
APPLICANT: Gemmill, Robert M.
APPLICANT: Drabkin, Harry A.
TITLE OF INVENTION: TRC8, A GENE RELATED TO THE HEDGEHOG RECEPTOR, PATCHED FILE OF INVENTION UMBER: US/09/268,140
CURRENT APPLICATION NUMBER: US 60/077,723
PRIOR APPLICATION NUMBER: US 60/077,723
PRIOR PILING DATE: 1998-03-12
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patent In Ver. 2.0
                                                                                                                                                                                                                                                                                        130 --SYLISKLRNYEKLHKRCGPGTESYKKALKQLDQEHIDGDGECKYVVWISFSGLGNRIL 187
                                                                                                                                                                                                        71 RIMGFAEARVLDAGVFPNVTNINSDKLLGGLLASGFDEDSCLSRYQSVHYRKPSFYKPS- 129
                                                                                                                                                                                                                                                                                                                                                                       188 SLASVFLYALLIDRVLLVDRGKDMD---DLFCEPFLGMSWLLPLDFPMTDQFDGLNQESS 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --- QTFIGKVP 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          294 WLIVKTDNYFVPSLWLIPGFDDELNKLFPQKATVFHHLGRYLFHPTNQVWGLVTRYYEAY 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218 PFLGMSW------QESSRCYGYM 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251 VKNQVIDTEGTLSH-LYLHLVHDYGDHDKMPFCEGDQTFIGKVPWLIVKTDNYFVPSLWL 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     310 IPGFDDELNKLFPQKATVFHHLGRYLFHPTNQVWGLVTRYYEAYLSHADEKIGIQVRVFD 369
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                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99; Indels 122;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3; Length 1286;
                                                                                                                              DB 2; Length 3778;
45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          245 RCYGYMVKNQVIDTEGTLSHLYLHLVHDYGDHDKMFFCEGD-
                                                                                                                                             Best Local Similarity 20.7%; Pred. No. 45;
Matches 67; Conservative 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.0%; Score 89.5; D
20.6%; Pred. No. 8.7;
tive 41; Mismatches
                                                                                                                              Score 90;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----DKSIGQQVHNSTSYVLNED 1750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             354 LSHADEKIGIQVR-----VFDED 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LENGTH: 1286
; TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-268-140-3
    3778 amino acids
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Best Local Similarity 20.6
Matches 64; Conservative
                       TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                     ; MODECULE IXE
US-08-222-617A-2
LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-268-140-3
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                                                                                                                            Query Match
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Best Local Similarity 20.3%; Pred. No. 9.8;
Matches 63; Conservative 39; Mismatches 83; Indels 126; Gaps 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421 GYAENLKSMY------WEYPTSTGEIIGVHQPSQEGYQQTEKKMHNGKAL----A 465
                                                   | :: | : | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
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STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
US-08-656-055-6
Sequence 6, Application US/08656055
Patent No. 6027882
GENERAL INFORMATION:
APPLICANT: SCOTT, MATHEW P
APPLICANT: GOORICH, LISA V
APPLICANT: GOORICH, LISA V
APPLICANT: GOORICH, LISA V
APPLICANT: JOHNSON, RONALD L
TITLE OP INVENTION: Patched Genes and their Use
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/656,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 370 EDPGPFQHVMDQISSCTQKEKLLPEVDT---
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REGISTRATION NUMBER: 20015
REFERENCE, DOCKET NUMBER: a60190-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94111
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/540,406
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1285 amino acids
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                                                                                                                                                                   466 EM--YLLSLTD 474
:| || || || 900 QMPFYLHGLTD 910
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MOLECULE TYPE: protein
US-08-656-055-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Four Embarca
CITY: San Francisco
STATE: CA
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STRANDEDNESS: sin
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791 E-----EYRDGRLTKECWFPNASSDAILAYKLIVQTGHVDNPVDKELVLTNRLVNS 841

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Sequence 815, App
Sequence 504, App
Sequence 303, App
Sequence 304, App
Sequence 104, App
Sequence 2315, A
Sequence 2315, A
Sequence 2315, A
Sequence 68, Appl
                                                                                                                                                   ; Search time 39 Seconds
(without alignments)
2973.483 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 152, A
Sequence 612, A
Sequence 835, A
Sequence 504, A
Sequence 305, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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3004
1 MDONSYRRRSSPIRTITGGS......GTLVPHVRHCEDISWGLKLV 558
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_MEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/PCT_MEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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9: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-194A-152
US-09-882-227-612
US-10-238-075-835
US-10-032-2018-305
US-10-032-2018-305
US-10-032-2018-304
US-10-032-2018-304
US-10-363-493-19663
US-10-369-493-19663
US-10-253-007-58
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US-10-369-493-646
US-09-843-905A-6
US-10-317-250-6
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Maximum Match 100%
Listing first 45 summaries
                                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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	Sequence 6478, Ap Sequence 11, Appl Sequence 2460, Ap Sequence 7524, Ap			Sequence 107, App Sequence 16, Appl Sequence 105, App Sequence 6312, Ap Sequence 7655, Ap	Sequence 4, Appli Sequence 1, Appli Sequence 2, Appli Sequence 7407, Ap Sequence 8043, Ap Sequence 10263, A
	US-10-369-493-6478 US-10-317-832-11 · US-10-104-047-2460 US-10-032-585-7524		US-10-421-446-6 US-10-041-030-4 US-10-197-666A-136 US-10-128-714-3043	US-10-120-801-107 US-10-120-608-16 US-10-370-685-105 US-10-369-493-6312 US-10-032-585-7655 US-00-793-705-6	US-09-813-905A-4 US-10-317-250-4 US-10-443-108-10 US-10-041-030-2 US-10-032-585-7407 US-10-128-714-8043 US-10-369-493-10263 US-09-815-242-12623
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Sequence 35, Application US/10338777
Publication No. US20030188343A1
Reneabla INFORMATION:
APPLICANT: Lynx Therapeutics, Inc.
APPLICANT: United States Department of Agriculture
APPLICANT: Haudenschild, Christian D
APPLICANT: Haudenschild, Christian D
APPLICANT: Bowen, Benjamin A
APPLICANT: Buckler, Edward S
TITLE OF INVENTION: Identification of Genes Associated with Growth in Plants
FILE REFREENCE: 37-00510US
CURRENT APPLICATION NUMBER: US/10/338,777
CURRENT FILING DATE: 2003-01-07
NUMBER OF SEQ ID NOS: 405
SOFTHAMRE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 HKRCGPGTESYKKALKQLDQEHI-DGDGECKYVVWISFSGLGNRILSLASVFLYALLTDR
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49.7%; Score 1492; DB 12;
Best Local Similarity 54.6%; Pred. No. 7.6e-147;
Matches 295; Conservative 90; Mismatches 133;
ALIGNMENTS
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: LENGTH: 533

: TYPE: RRT

: ORGANISM: Arabidopsis thaliana

US-10-338-777-35
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                                                FLGMSWLLPLDFPMTDQFDGLNQESSRCYGYMVKNQVI-
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17.8%; Pred. No. 0
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NUMBER OF SEQ ID NOS: 638
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 612
LENGTH: 658
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Publication No. US20030158396A1
GENERAL INFORMATION:
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                                                                                 230 SIPPHLYMHNLHDSRDSDKLFVCQKDQSLIDKVPWLIVQANVYFVPSLWFNPTFQTELVK 289
                                                                                                                                           GTLSHLYLHLVHDYGDHDKMFFCEGDQTF1GKVPWLIVKTDNYFVPSLWLIPGFDDELNK 319
                                                                                                                           LFPQKATVFHHLGRYLFHPTNQVWGLVTRYYEAYLSHADEKIGIQVRVFDEDPGPFQHVM 379
                                                                                                                                                                                        DQISSCTQKEKLLPEVDTLVERSRHVN-TPKHKAVLVTSLNAGYAENLKSMYWEYPTSTG 438
                                                                                                                                                                                                                                                   EIIGVHQPSQEGYQQTEKKMHNGKALAEMYLLSLTDNLVTSAWSTFGYVAQGLGGLKPWI 498
                                                                                                                                                                                                                                                                                                                  LYRPENRTTPDPSCGRAMSMEPCFHSPPFYDCKAKTGIDTGTLVPHVRHCEDISW-GLKL 557
 VLLVDRGKDMDDLFCEPFLGMSWLLPLDFPMTDQFD--GLNQESSRCYGYMVKNQVIDTE 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QLDQEHIDGDGECKYVVWISFSGLGNRILSLASVFLYALLIDRVLLVDRGKDMDDLFCEP 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moughamer, Todd
Provart, Nicholas
Ricke, Darrell
Alu, Tong
FENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF FILE REFERENCE: 70029-NP
CURRENT APPLICATION NUMBER: US/10/259,194A
CURRENT FILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR APPLICATION NUMBER: US 60/370,743
PRIOR APPLICATION NUMBER: US 60/370,743
PRIOR FILING DATE: 2002-04-04
PRIOR FILING DATE: 2002-04-04
PRIOR PLING DATE: 2002-04-04
PRIOR FILING DATE: 2002-04-04
PRIOR PLING DATE: 2002-04-04
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40.8%; Pred. No. 1.2e-94;
tive 76; Mismatches 194; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glazebrook, Jane
Goff, Stephen A.
Katagiri, Fumiyaki
Kreps, Joel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lange, Markus B.
APPLICANT: Ghassemian, Majid
APPLICANT: Briggs, Steven P.
APPLICANT: Cooper, Bret
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Best Local Simi
Matches 223;
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APPLICANT: Al-Garawi, Amal
APPLICANT: All-Garawi, Amal
APPLICANT: Miler, Charles
APPLICANT: Miler, Charles
APPLICANT: Jobb, Jean-Francois
APPLICANT: Ocomen, Raymond P.
TITLE OF INVENTION: Encoding No. US20030158396A1e1 Helicobacter Polypeptides in the JITLE OF INVENTION: Encoding No. US20030158396A1e1 Helicobacter Polypeptides in the JITLE OF INVENTION: Genome
FILE REFERENCE: 06132/047002
CURRENT APPLICATION NUMBER: US/09/882, 227
CURRENT FILLING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 08/902, 615
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264
                                297 PAYVYLSLGYQMADKLFFCGDDQRALAKVNWLLLYSDLYFVPSLYSVAEFNGELRRLFFPA 356
                                                                                                                                                                                                                                                                                 412 ---TGKPPPDNDNDDDLATAYDS--NSSNGSGGGNYSAILIASLYPDYYERIRATYYEHA 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     526
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                                                                                                                                                                                                                                                                                                                                                                             383 SSCTQK-----EKLLPEVDTLVERSRHVNTPKHKAVLVTSLNAGYAENLKSMYWEYP 434
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                                                                                                                      -LYLHLVHDYGDHDKMFFCEGDQTFIGKVPWLIVKTDNYFVPSLWLIPGFDDELNKLFPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       495 KPWILYRPENRTTPDPSCGRAMSMEPCFHSPPFY---DCKAKTG-IDTGTLVPHVRHCED
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Sequence 305, Application US/10032201B Publication No. US2030167524A1 GENERAL INFORMATION: APPLICANT: Van Rooijen, Gijs
       Sequence 504, Application US/09934455
Publication No. US20030121070A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-934-455-504
                                                     APPLICANT: Adam, Luc
APPLICANT: Creelman, Robert
APPLICANT: Dubell, Arnold
APPLICANT: Heard, Jacqueline
APPLICANT: Jiang, Cai-Zhong
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Publication No. US20030148324A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: B. COLI, and blological uses of these polynucleotides and of their FILE OF INVENTION: B. COLI, and blological uses of these polynucleotides and of their FILE REFERENCE: BLANDINE
CURRENT APPLICATION NUMBER: US/10/238,075
CURRENT APPLICATION NUMBER: 000145
PRIOR APPLICATION NUMBER: 00001310
NUMBER OF SEC ID NOS: 1576
SOFTWARE: Patentin version 3.1
SEC ID NO 835
                             176 TEVEKQEDFYNQYWRAMEERPEQNETLFNRFVRHYLTIKIGKIPNEKRVYEAFKDYRQKK 235
                                                                                                                                     277 DKMFFCEGDQTFIGKVPWLIVKTDNYFVPSLWLIPGF------DDELNKLFP---- 322
                                                                                                                                                             323 --QKATVFHHLGRYLF-----HPTNQVWGLV------TRYYEAYLSHADEKIG 362
                                                                                                                                                                                                                                                                              363 IQVRVFDEDPGPFQHVMDQISSCTQXEKLLPEVDTLVERSRHV--NTPKHKAVLVTSLNA 420
                                                                                                                                                                                                                                     336 HIQKDEYFKSLKAHFVCLTEKQRPPNNDEFKKLFITIDFYKFKKNKYFLERLENFDTKEP 395
                                                                                                                                                                                                                                                                                                               396 V-----DIQKCNIEHIMPQILITPEWQRDLGENFQAIHEKYLHTIGN-----LILITGYNS 444
                                                                                                                                                                                                                                                                                                                                                                                        445 KYSNNSFQEKRDMEKGFKQSSLKLNQSLKDLESFGEKRIEKRASDLADWALKIWTYPILE 504
                                                                                                                                                                                                                                                                                                                                                            -----YWEYPTST 437
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253 TIYGEIVGFATNCDAAHITQPQRETMQYCMEQSLKIAGLSAQDIGYISAHGTATDRGDMA 312
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                                                                    237 ---- DGLNQESSRCYGYMV----KNOVIDTEGTLSH-
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206 DRGKDMDDLFCEPFLGMSWLLPLDFPMTDQF
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ORGANISM: Escherichia coli
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RESULT

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66 PSDSNRIMGFAEARVLD-----AGVFP----NVTNINSDKLLGGLLASGFDE---- 108
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3.3%; Score 99; DB 11; Length 76
Best Local Similarity 21.8%; Pred. No. 1.2;
Matches 85; Conservative 54; Mismatches 173; Indels
APPLICANT: Keddie, James
APPLICANT: Ratcliffe, Oliver
APPLICANT: Ratcliffe, Oliver
APPLICANT: Ratcliffe, Oliver
APPLICANT: Ricchmann, Jose Luis
APPLICANT: Ricchmann, Jose Luis
APPLICANT: Yu, Guo-Liang
APPLICANT: Pineda, Omaira
TITLE OF INVENTION: Genes for Modifying Plant Traits IV
FILE REPERENCE: MBI-0025
CURRENT APPLICATION NUMBER: US/09/934,455
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PRIOR APPLICATION NUMBER: 60/227439
PRIOR PILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: MBI-0023
PRIOR PILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 516
SOFTWARE: PATCHIN VERSION 3.1
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83

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APPLICANT: Briggs, Steven
APPLICANT: Dalmia, Bipin Kumar
APPLICANT: Dalmia, Bipin Kumar
APPLICANT: Dalmia, Bipin Kumar
APPLICANT: Dalmia, Bipin Kumar
APPLICANT: Zaplachinski, Steve
APPLICANT: Zaplachinski, Steve
APPLICANT: Moloney, Maurice
TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
TITLE OF INVENTION: COMPOSITIONS
FILE REFERRICE: 38814 3518
CURRENT APPLICATION NUMBER: US/10/032,2018
CURRENT FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 313
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                                                                                                                                                                                                                                                                                                                 285 KKL---PTNQL-----QVTWEDHASGK------EDTGTFDTVLWAIGR----- 318
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                                                   Length 524;
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21.2%; Pred. No. 1.3;
[ve 40; Mismatches 99; Indels
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                                                   3.2%; Score 96; DB 12;
21.2%; Pred. No. 1.3;
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319 VPETRTLNLEKAGISTNPKNQKIIVDAQEA------
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                                                                                                    40; Mismatches
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CTHER INFORMATION: Xaa = Any Amino Acid
US-10-032-201B-304
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APPLICANT: Van Rooijen, Gijs
APPLICANT: Deckers, Harm
APPLICANT: Heifetz, Peter Bernard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.2%;
Best Local Similarity 21.2%;
Matches 58; Conservative 4
                                                                         Best Local Similarity 21.2
Matches 58; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: VARIANT
JS-10-032-201B-303
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                                                      Query Match
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                                                              APPLICANT: Dalmia, Bipin Kumar
APPLICANT: Dalmia, Bipin Kumar
APPLICANT: Dal Val, Greg
APPLICANT: Dal Val, Greg
APPLICANT: Applachinski, Steve
APPLICANT: Moloney, Maurica
TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
TITLE OF INVENTION: COMPOSITIONS
TITLE OF INVENTION: COMPOSITIONS
TITLE OF INVENTION WINDER: US/10/032,201B
CURRENT APPLICATION NUMBER: US/10/032,201B
CURRENT FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 313
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 305
LENGTH: 520
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APPLICANT: Heiferz, Peter Bernard
APPLICANT: Heiferz, Peter Bernard
APPLICANT: Heiferz, Peter Bernard
APPLICANT: Briggs, Bipin Kumar
APPLICANT: Dalmia, Bipin Kumar
APPLICANT: Dalmia, Steve
APPLICANT: Zaplachinski, Steve
APPLICANT: Zaplachinski, Steve
APPLICANT: Moloney, Maurice
TITLE OF INVENTION: COMPOSITIONS
TITLE OF INVENTION: COMPOSITIONS
FILE REPERENCE: 38814 3518
CURRENT APPLICATION NUMBER: US/10/032,2018
CURRENT APPLICATION NUMBER: US/10/032,2018
WUMBER OF SEQ ID NOS: 313
SOFTWARE: FREESEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 12; Length 520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 3.2%; Score 96; DB 12; Length 520 Best Local Similarity 21.2%; Pred. No. 1.3; Matches 58; Conservative 40; Mismatches 99; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            500 ----YRPENRTTPDPSCGRAMSMEPCFHSPP 526
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LOCATION: 523
OTHER INFORMATION: Xaa = Any Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 303, Application US/10032201B Publication No. US20030167524A1 GENERAL INFORMATION:
                           Peter Bernard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Van Rooijen, Gijs
                                                   Briggs, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Mus musculus
US-10-032-2018-305
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ORGANISM: Mus musculus
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IN PLANTS FOR PRODUCTION

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APPLICANT: Cao, Yongwei
APPLICANT: Gao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 SGFDEDSCLSRYQS----VHY----
                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-22315
                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                               SEQ ID NO 22315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-253-007-58
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                                                                                                                                                                                                                                             APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF FILE REFERENCE: 38-10(52052)8
CURRENT FILING DATE: 2003-02-28
PRIOR PILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
LENGTH: 934
                          369 PELTPTAIKAĞKLLAQRLFGKSSTLMDYSNVPTTVFTPLEYGCVGLSEEEAVALHGQEHV 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 LRNYEKLHKRCGPGTESYKKALKQLDQEHIDGDGECKYVVWI------SFS--- 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  481 DVTQCELRILKWAAEIQRRFGHAALPNYIISMATGVVHILEVALLLKEAGLLQFGDD--- 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       214 LFCEPFLGMSWLLPLDFPMTDQFDGLNQESSRCYGYMVKNQVIDTEGTLSHLYLHLVHDY 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334 YLFHPTNOVWGLVTR----YYEAYLSHADEKIGIQVRVFDE------DPGPFQHVMD 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       622 RLFHGRG---GTVGRGGGPSYQGILAQPPGSVSGQIRLTEQGEVIASKYTDPEIGRRNLE 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QISSCTQKEKLLPEVDTLVERSR-HVNTPKHKAV---LVTSLNAGYAE-----NLKSMY 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | :| :| :| :| :| :| :| 588 SDSNK-----HGVRL 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          679 TLVAATIE----STLLDRDAVHYHAPHYHQIMEELSSACAAYRDLVYKTPGFKQFF 731
451 YQQTEKKMHNGKALAE-MYLLSLT----DNLVTSAWSTFGYVAQGLGGLKPWIL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 -----DRVLLVDRGKDMDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 3.2%; Score 96; DB 12; Length 934;
Best Local Similarity 19.5%; Pred. No. 3.3;
Matches 81; Conservative 68; Mismatches 146; Indels 120;
                                                                                                  EVYHAYYKPLEFTVADRDASQCYIKMVCMREPP 461
                                                                       ----YRPENRITPDPSCGRAMSMEPCFHSPP 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: unsure
: LOCATION: (1)..(934)
: OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-19663
                                                                                                                                                                                              Sequence 19663, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
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----RKPSPYKPSSYLISKL 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137 RNYEKLHKRCGPGTESYKKALKQLDQEHIDGDGECKYVVWISFSGLGNRILSLASVFLYA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          276 ES-------SYTEVTKLLKNEGIDLDHK-----RFLILOGEVENIAQMKPKA 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197 LLTDRVLLVDRGKDMDD---LFCEPFLGMSWLLPLDFPMTDQFDGLNQESSRCYGYMVKN 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            254 QVIDTEGTLSHLYLHLVHDYGDHDKMFFCEGDQTFIGKVPWLIVKTDNYFVPSLWLIPGF 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            362 BIVDREKNSL-----ESGKETALEFLEKEK-----------------------391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---RSKLFQFK------LLQSNSKLASTLEKISSSNKDLEDEKMKFQESLKKVDEI 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGPFQHVMDQISSCTQKEKLL----PEVD----TLVERSRHVNTPKHKA---VLVTSLNA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421 GYAEN----LKSMYWEYPISTGEIIGVHQPSQEGYQQTEKKWHNGKALAEMYLLSLTDNL 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DHKSYSQ--SPPRSP--GRSPTRRLELLQLSPVKNSRVELQKIYDRHQSSSKQQSRLFIN
                                                                                                                                                                                                                                    48 CLIV--FSVLVAFSMIFHQHPSDSNRI--MGFAEARVLDAGVFPNVTNINSDKLLGGLLA
                                                                                                                                                                                                                                                                            ----TRTFTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
Ouery Match
3.1%; Score 93; DB 12; Length 1418;
Best Local Similarity 19.3%; Pred. No. 13;
Matches 110; Conservative 86; Mismatches 208; Indels 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Benfey et al. TITLE OF INVENTION: Scarecrow Gene, Promoter and Uses
                                                                                                                   DONSYRRESPIRTTGGSKSVNFSELLOMKYLSSGTMKL
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; Publication No. US20030088073A1
; GENERAL INFORMATION:
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371

RESULT 10 US-10-369-493-22315 ; Sequence 22315, Application US/10369493

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Query Match
Best Local Similarity
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SEQ ID NO 19347
LENGTH: 946
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Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                66 PSDSNRIMGFAEARVLD-----AGVFP----NVTNINSDKLLGGLLASGFDE---- 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSCLSRYQSVHYRKPSPYKPSSYLIS-KLRNYEK-LHKRCGPGTESYKKALKQLDQEHI- 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -- DGDGECKYVVWISFSGLGNRILSLASVFLYALLTDRVLLVDRGKDMDDLFCEPFLGMS 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WL---LPLDFPMTDQFDGLNQESSRCYGYMVKNQVIDTEGTLSHLYLHLVHDYGDHDKMF 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DŚVLKYISQVLMEEDMEEKPCMFHDALALQAAEKSLYEALGEKDPSSSSASSVDHPERLA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 SHSPDGSCS-----GGAPSDYAS-----TTTTTSSDSHWSVDGLENRP----S 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FCEGDQ---TPIGKVPWLIVKTDNYFVPSLWLIPGFDDBLNKLF---PQKATVFHHLGRY 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          335 LFHPTNQVWGLVTRYYEAYLSHADEKIGIQVRVFDEDPGPFQHVMDQISSCTQKEKLLPE 394
                                                                                                                                                                                                                                                                                                                                                                             3.1%; Score 92; DB 15; Length 809;
21.7%; Pred. No. 6.9;
ive 52; Mismatches 179; Indels
            FILE REFERENCE: 5914-074-999
CURRENT APPLICATION NUMBER: US/10/253,007
CURRENT TLING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: US/09/186,188
PRIOR PILING DATE: 1998-11-05
PRIOR APPLICATION NUMBER: 08/842,445
PRIOR APPLICATION NUMBER: 08/842,445
PRIOR APPLICATION NUMBER: 08/638,617
PRIOR PILING DATE: 1996-04-26
PRIOR PILING DATE: 1996-04-26
NUMBER OF SEQ ID NOS: 79
SOFTWARE: FABELSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           395 VDTLVERSRHVNTPKHKAVLVTSLNAG 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----ILNQNFPTESAKVVTAQSNG 408
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CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                         ; NAME/KEY: VARIANT
; LOCATION: (1)...(809)
; OTHER INFORWATION: Xaa = Any Amino Acid
US-10-253-007-58
Thereof
                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 21.7
Matches 84; Conservative
TITLE OF INVENTION:
                                                                                                                                                                                                                                                         ORGANISM: Plant
                                                                                                                                                                                                        SEQ ID NO 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Blatch, Gregory J.
APPLICANT: Blatch, Steven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052)8
FILE REFERENCE: 38-10 (52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
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                                                                                                                                                                                                                                                                                                                                                                                                 79 RVLDAGVFPNVTNINSD-----KLLGGLLASGFDED----SCLSRYQSVHYRKPS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                              421 QMLDIPVF----HVNGDDPEACVHIAKLVAEYRQT-FKSDVVIDLVCYRRYGHNEGDEPS 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 PYKPSSYLI-----SKLRNYEKLHKRCGPGTESYKKALKQLDQEHID----G 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210 DMDDLFCEPFLGM-----SWLLPLDFPMTDQFDGLNQESSRCYGYMVKNQVIDTE-GTL 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      323 QKATVFHHLGRYLFH----PINQVWGLVTRYYBAYLSHADEKIGIQVRVFDEDPGPFQHV 378
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                                                                                                                                                                                                                                                                 78
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                                                                                                                                Query Match 3.1%; Score 92; DB 12; Lengtn 940; Best Local Similarity 21.7%; Pred. No. 8.9; Matches 105; Conservative 63; Mismatches 166; Indels 150;
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Pred. No. 4.4;
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Publication No. US20030233675A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Deinococcus radiodurans
US-10-369-493-646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.0%;
TYPE: PRT; ORGANISM: Myxococcus xanthus US-10-369-493-19347
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SEQ ID NO 646
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----NLKSMY- 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --VD----TLVERSR----HVNTPKHKAVLVTSLNAGYAE-------NLKSMY- 430
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                                                                                               357 ADEKIGIQVR-----VPDEDPGPFQHV-----MDQISSCTQKEKLLPE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 419;
                                                                                                                                                                                                                 395 --VD----TLVERSR----HVNTPKHKAVLVTSLNAGYAE-----
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19.2%; Pred. No. 3.4;
tive 42; Mismatches
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US-10-317-250-6
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Best Local Similarity
Matches 61; Conserva
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US-10-317-250-6
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      20;
                                                                                                  170 LKFPDLIHSQKPSPTTNIQSQERIFDFPAGSPEATHMITLLYSFWGIPASYRFMQ---- 224
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                                                            54 VLVAPSMIFH--QHPSDSNRIMGPAEARVLDAGVFPNVTNINSDKLLGGLLASGFDEDSC 111
                                                                                                                                                                                     -----YK----PSSYLISKLRNYE 140
                                                                                                                                                                                                                                                                                                       141 KLHKRCGPGTESYKKALKQLDQEHIDGDGECKYVVWISFSGLGNRILSLASVFLYALLTD 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -TNOVWGLV-- 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        345 FGTGVLVDGLDFSDDKMLQGRTFSYSDTQRYRVGPNYLQLPINAPKKHVATNQRDGQMAY 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       347 -----TRYYEAYLS------HADEKIGIQVRVFDEDPGPPQHVMDQISS 384
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   43; Mismatches 177; Indels 184; Gaps
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3.0%; Score 90.5; DB 10;
Best Local Similarity 19.2%; Pred. No. 3.4;
Matches 61; Conservative 42; Mismatches 96;
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Sequence 6, Application US/09843905A

Sequence 6, Application US/09843905A

GENERAL INFORMATION:
APPLICANT: Bird, Timothy A.
APPLICANT: Cosman, David J.
TITLE OF INVENTION: HUMAN PELLINO POLYPEPTIDES
FILE REFERENCE: 2990-A

CURRENT APPLICATION NUMBER: US/09/843,905A

CURRENT FILING DATE: 2001-04-27

PRIOR FILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin version 3.1

SEQ ID NO 6
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                                                                                                                                                                              112 LSRYQSVHYRKPSP------
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ORGANISM: Mus musculus
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